

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 3, 2000, 14:19:01 ; Search time 33043.4 Seconds
(without alignments)
141.116 Million cell updates/sec

Title: US-08-962-560a-3
Perfect score: 1235
Sequence: 1 CGAGGCTCAAGCTCCGGCGC.....ACAAAAAAAAAAAAAAAA 1235

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4538634 seqs, 1887831982 residues

Total number of hits satisfying chosen parameters: 9077268

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : EST:
1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
13: em_est13:*
14: em_est14:*
15: em_est15:*
16: em_est16:*
17: em_est17:*
18: em_est18:*
19: em_est19:*
20: gb_est1:*
21: gb_est2:*
22: gb_est3:*
23: gb_est4:*
24: gb_est5:*
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84: em_gss2:*
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99: em_gss10:*
100: em_gss11:*
101: em_gss12:*
102: gb_gss12:*
103: gb_gss13:*
104: gb_gss14:*
105: gb_gss15:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Match Length	DB	ID	Description
1	574.8	46.5	602	39	AA881502 vx19f05.r
2	511.2	41.4	623	39	AA849015 EST191777


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Db      482  TCGCAGGAGAGCTCTTTCGGGCTCAGAGTGAAGATGCTTCGGGCGCCAGAGCAT 541
OY      541  CCGCGTGCATTTCCAGGCGCGCGCTTCACCTTGAGAGCGGCGGAGACCTTCGACTG 600
Db      542  CCGCGTGCATTTCCAGGCGCGCGCTTCACCTTGAGAGCGGCGGAGACCTTCGACTG 601
OY      601  C 601
Db      602  C 602

RESULT  2
LOCUS   AA849015      623 bp      mRNA      EST      30-APR-1998
DEFINITION EST191777 Normalized rat lung, Bento Soares Rattus sp. cDNA clone
LOCUS    RLU0A34.3' end, mRNA sequence.
ACCESSION AA849015
VERSION    AA849015.1 GI:2936555
KEYWORDS   EST.
SOURCE     Rattus sp.
ORGANISM   Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 623)
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (RESE) Catalog & Rat
Gene Index
Unpublished (1998)
On Jan 9, 1998 this sequence version replaced gi:936155.
Contact: Lee, NH
ATCC
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.

FEATURES
source
1..623
/organism="Rattus sp."
/db_xref="ATCC (inhost):2008043"
/db_xref="taxon:10118"
/clone="RLU0A34"
/clone_1lb="Normalized rat lung, Bento Soares"
/notes="Organ: Lung; Vector: pT73Pac; Site_1: EcoRI;
Site_2: NotI"
BASE COUNT 94 a 193 c 254 g 82 t
ORIGIN
Query Match 41.4%; Score 511.2; DB 39; Length 623;
Best Local Similarity 91.1%; Prid. No. 2.9e-85;
Matches 543; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

OY      56  TGGCGGCGCTGTCGACACCGGAGCGCGGCTCCTGCTGCCCATGAGCGCAG 115
Db      596  TGGCGGCGACACCGCGGAGACCGCGCGCGCGCGCTCCGCGCGAGCGCAG 537
OY      116  CCGCGAGCATATGAGCCACCTCCAGCTGAGCCCTCGATGATGATGATGATGATGATGAT 175
Db      536  CCGCGAGCATATGAGCCACCTCCAGCTGAGCCCTCGATGATGATGATGATGATGATGAT 477
OY      176  CAGGTGGCAGCCGACAAATGCGATCTCCCGGCGAGCAGAGCGCGCGGTGAGAGCCC 235
Db      476  CAGGTGGCAGCCGACAAATGCGATCTCCCGGCGAGCAGAGCGCGCGGTGAGAGCCA 417
OY      236  TCGTGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 295
Db      416  TCGTGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 357
OY      296  GTCCAGAGCCCGACCCCTGCGAGACTTCCGACCTTCCGCTCCGCTCCGATTAAC 355

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Db      356  GTCCGCGCCCGGCTCCGCGGAGACACTTCCGACCTTCGCTCCGACCTGATTAAC 297
OY      356  CCGCGCATCACGGGAGACACGCGCTCTCTGAGAGCGCTTCATATTGGAGCCCTG 415
Db      296  CCGCGCATCACGGGAGACACGCGCTCTCTGAGAGCGCTTCATATTGGAGCCCTG 237
OY      416  AGCGTGCAGCGGCGGAGACGAGCGGCTGCGGAGCGCGGAGCGGACCTTCTGATGCGC 475
Db      236  AGCGTGCATGCGGCGGAGACGAGCGGCTGCGGAGCGCGGAGCGGACCTTCTGATGCGC 177
OY      476  GACAGTGCATCACGGAATCTCTTCGCGCTCAGCGTGAAGATGCTTGGGCGCCACG 535
Db      176  GACAGTGCAGCGGAGAACTCTTCTGCGCTCAGCGTGAAGATGCTTGGGCGCCACG 117
OY      536  AGCATCCGCGCTGACCTTCACGCGCGCGCTTCACCTTGAGAGCGGCGGAGACCTTC 595
Db      116  AGCATTCGTGTGCACTTCACGCGCGCGCTTCACCTTGAGAGCGGCGGAGACCTTC 57
OY      596  GACTGCTTTGAGGCTGCTGAGAGCACTACGTGCGGCGCGCGCGCGCATGTTGGG 651
Db      56  GACTGCTTTCGAGCTGCTGAGAGCACTACGTGCGGCGCGCGCGCATGTTGGG 1

RESULT  3
LOCUS   A1019717/c      538 bp      mRNA      EST      16-JUN-1998
DEFINITION ua94b12.r1 Soares mouse mammary gland NBMWG Mus musculus cDNA clone
LOCUS    IMAGE:1365119 5' similar to TR:035716 035716 SUPPRESSOR OF CYTOKINE
SIGNALLING-1. [1] ; mRNA sequence.
ACCESSION A1019717
VERSION    A1019717.1 GI:3234053
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 538)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theisling,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
On Jan 17, 1998 this sequence version replaced gi:2044043.
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:898339
Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 512.

FEATURES
source
1..538
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1365119"
/clone_1lb="Soares mouse mammary gland NBMWG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/notes="Organ: mammary gland; Vector: pT73D-Pac
(pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5]"

```

TGTACCAATCTGAAGTGGAGGCGCGGCGGAGGATGTTTATTTTATTTTATTTT
 T 3'): double-stranded cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of the modified p773 vector.
 RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
 constructed and normalized by Bento Soares and M. Fatima
 Bonaldo."

BASE COUNT 161 a 137 c 150 g 90 t
 ORIGIN

Query Match 41.1%; Score 508.2; DB 41; Length 538;
 Best Local Similarity 99.2%; Pred. No. 1e-84;
 Matches 521; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 686 CAGGACTGTGTGCGCAGGATCGTGGCGCGGTGGCGAGAACCTGGCGGCATC 745
 DB 538 CAGGACTGTGTGCGCAGGATCGTGGCGCGGTGGCGAGAACCTGGCGGCATC 479
 QY 746 CCTTACACCGGTACTCGGTGACTACCTGAGTTCCTCCCTCCAGATGACCGGCT 805
 DB 478 CCTTACACCGGTACTCGGTGACTACCTGAGTTCCTCCCTCCAGATGACCGCT 419
 QY 806 GCGCTGTGCGCAGGATTAAGTGGGCGCGCTTATTTATTTATTTATTTATTT 865
 DB 418 GCGCTGTGCGCAGGATTAAGTGGGCGCGCTTATTTATTTATTTATTTATTT 359
 QY 866 ATTTTCTGAGAACAGTGGAGACCTCCCGCTGGTGGAGAGAGTGTGTGAGG 925
 DB 358 ATTTTCTGAGAACAGTGGAGACCTCCCGCTGGTGGAGAGAGTGTGTGAGG 299
 QY 926 GTGAGATGCTCCCATCTTCGCTGAGAGACCTCATCCACCTCAGGGGTGGTGTCT 985
 DB 298 GTGAGATGCTCCCATCTTCGCTGAGAGACCTCATCCACCTCAGGGGTGGTGTCT 239
 QY 986 CCCCTCTGCTGCTCCCTCCCGGCTCCCGCTGGTGTGAGAGCTGTGTGTGGGCGAG 1045
 DB 238 CCCCTCTGCTGCTCCCTCCCGGCTCCCGCTGGTGTGAGAGCTGTGTGTGGGCGAG 180
 QY 1046 ACCTGAATCCATCTCTACCTCCAGTGTATATTCACATCTTGCAGCAACCA 1105
 DB 179 ACCTGAATCCATCTCTACCTCCAGTGTATATTCACATCTTGCAGCAACCA 120
 QY 1106 GGGGTGGGAGAGGCTCTGCTTCAATTTTCTGCTGAGAGATATCCATTTTATTT 1165
 DB 119 GGGGTGGGAGAGGCTCTGCTTCAATTTTCTGCTGAGAGATATCCATTTTATTT 60
 QY 1166 TTTCACGACGATTAGATTAATACTTATTAATAAGTTTATTT 1210
 DB 59 TTTCACGACGATTAGATTAATACTTATTAATAAGTTTATTT 15
 RESULT 4
 AA288982 517 bp mRNA EST 14-APR-1997
 LOCUS v04e05.r1 Soares mouse lymph node NBLN Mus musculus cDNA clone
 DEFINITION IMAGE:752192.5', mRNA sequence.
 ACCESSION AA288982
 VERSION AA288982.1 GI:1936171
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 517)
 AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisler, S., Kucabara, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT On Sep 12, 1996 this sequence version replaced gi:1404954.

Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:461176
 Seq primer: -28m13 rev2 ET from Amersham
 High quality sequence stop: 475.
 FEATURES
 source
 1..517
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_image="IMAGE:752192"
 /clone_lib="Soares mouse lymph node NBLN"
 /sex="male"
 /tissue_type="lymph node"
 /dev_stage="4 weeks"
 /lab_host="DH10B"
 /note="Organ: lymph node; Vector: p773D-Pac (Pharmacia)
 with a modified polylinker; Site 1: Not I; Site 2: Eco RI;
 1st strand cDNA was primed with a Not I - oligo(dT) primer
 15'.
 TGTACCAATCTGAAGTGGAGGCGCGGCGGAGGATGTTTATTTTATTTTATTTT

BASE COUNT 156 a 130 c 142 g 89 t
 ORIGIN

Query Match 41.0%; Score 506; DB 31; Length 517;
 Best Local Similarity 99.8%; Pred. No. 2.7e-84;
 Matches 517; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 700 CCAGGCGATCTGCGCGCGCGGTGGTGGAGAACCTGGCGGCATCTTACCCGCT 759
 DB 517 CCAGGCGATCTGCGCGCGCGGTGGTGGAGAACCTGGCGGCATCTTACCCGCT 458
 QY 760 ACTCGTGAATCTGAGTCTCTCCCTCCAGATCTGACCGGCGGTGGCGGCA 819
 DB 457 ACTCGTGAATCTGAGTCTCTCCCTCCAGATCTGACCGGCGGTGGCGGCA 398
 QY 820 GCATTAGTGGGCGCGCTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 879
 DB 397 GCATTAGTGGGCGCGCTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 338
 QY 880 ACCTGGAGACCTCCCGCGCTGGTGGAGAGTGTGTGGAGGTGAGATGCTCC 939
 DB 337 ACCTGGAGACCTCCCGCGCTGGTGGAGAGTGTGTGGAGGTGAGATGCTCC 278
 QY 940 ACTTCTGCTGAGACCTCATCCACCTCTCAGGGGTGGGCTGCTCCCTCTGTGT 999
 DB 277 ACTTCTGCTGAGACCTCATCCACCTCTCAGGGGTGGGCTGCTCCCTCTGTGT 218
 QY 1000 CCTCGGAGTCCCGCTGGTGTGACAGTGTGTCTGGGCGAGACCTGATTCACAT 1059
 DB 217 CCTCGGAGTCCCGCTGGTGTGACAGTGTGTCTGGGCGAGACCTGATTCACAT 159
 QY 1060 CCTACTCTCATGTTTATCATATTCAGATCTTGCAGCAACAGGGGTGGGAGG 1119
 DB 158 CCTACTCTCATGTTTATCATATTCAGATCTTGCAGCAACAGGGGTGGGAGG 99
 QY 1120 TCTCTGCTTCAATTTTCTGCTGCTGAGATATCTTATTTATTTATTTATTTATTT 1179
 DB 98 TCTCTGCTTCAATTTTCTGCTGCTGAGATATCTTATTTATTTATTTATTTATTTATTT 39


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/clone="IMAGE:1265184"
/sex="male" Soares 2NDMT"
/issue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TCCTACCACTCTGAGTGGAGGCGCCGCTTTTCTTTTCTTTTCTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT      157 a      129 c      138 g      87 t      1 others
ORIGIN

```

```

Query Match      38.5% Score 475.8; DB 39; Length 512;
Best Local Similarity 97.9%; Pred. No. 1e-78;
Matches 503; Conservative 0; Mismatches 8; Indels 3; Gaps 2;

```

```

OY 701 CAGCGCATCTGCGCCGCGGTCGCGAGAGACCTGGCGCATCCCTTAACCCGATA 760
|||||
DB 512 CAGCGCATCTGCGCCGCGGTCGCGAGAGACCTGGCGCATCCCTTAACCCGATA 453
|||||
OY 761 CTCGCTACTACTGAGTCTCTCCCTTCGAGATCGACCGGCTGCCGCTCCGAG 820
|||||
DB 452 CTCGCTACTACTGAGTCTCTCCCTTCGAGATCGACCGGCTGCCGCTCCGAG 393
|||||
OY 821 CATTAAGTGGGGGCGCTTATTTCTTATTAATTAATTAATTTTCTGGAACA 880
|||||
DB 392 CATTAAGTGGGGGCGCTTATTTCTTATTAATTAATTAATTTTCTGGAACA 333
|||||
OY 881 CGTGGAGCCCTCCCGCCCTGGTGCAGAGGAGTGTGTGGAGGATGAGATGCCCTCCA 940
|||||
DB 332 CGTGGAGCCCTCCCGCCCTGGTGCAGAGGAGTGTGTGGAGGATGAGATGCCCTCCA 273
|||||
OY 941 CTCTGCTGAGAGACCTATCCACCTCTCAGGGGTGGGG-GTCTCCCTCCCTGGTGTCT 999
|||||
DB 272 CTCTGCTGAGAGACCTATCCACCTCTCAGGGGTGGGGGTCTCCCTGGTGTCT 213
|||||
OY 1000 CCTCCGCGGTCGCCCTGGTGTGAGAGCTGTGTGCGGGCCAGACCTGAATTCACCT 1059
|||||
DB 212 CC--TCGCGTCCCCCGGTTGTGACAGCTGTGTCTGGGGCCAGGACCTGAATTCACCT 155
|||||
OY 1060 CCTACTCTCCAGTGTATTCATATTCAGATCTTTGACAAACAGAGGGGTGGGAGAGG 1119
|||||
DB 154 CCTACTCTCCAGTGTATTCATATTCAGATCTTTGACAAACAGAGGGGTGGGAGAGG 95
|||||
OY 1120 TCTCTGCTCATTTTCTCTGCTGTCGAGAAATTCCTATTTTATTTTACAGCACTTT 1179
|||||
DB 94 TCTCTGCTCATTTTCTCTGCTGTCGAGAAATTCCTATTTTATTTTACAGCACTTT 35
|||||
OY 1180 AGGTAATAAATTATATGAAAGTTTCTTTT 1213
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DB 34 AGGTAATAAATTATATGAAAGTTTCTTTT 1

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```

RESULT 7
LOCUS AI029171 548 bp mRNA EST 04-JUL-1999
DEFINITION UI-R-CO-1v-e-09-0-01.s1 UI-R-CO Rattus norvegicus cDNA clone
ACCESSION AI029171
VERSION AI029171.1 GI:4296711
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

```

```

REFERENCE 1 (Bases 1 to 548)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT On Jun 22, 1998 this sequence version replaced g1:3246997.
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: mssoares@blue.weeg.uiowa.edu

```

```

Oligo-dT track not found. Not I site shown in beginning of sequence
is likely internal to the message. cDNA library preparation: M.
Fatima Bonaldo, Ph.D. Clone distribution: clones will be available
through Research Genetics This clone is also available through the
I.M.A.G.E. Consortium at LBNL (info@image.lbnl.gov). IMAGE
ID=1782655 The following repetitive elements were found in this
cDNA sequence: 163-196, >AT-rich#low_complexity
Seq primer: M13 Forward
POLYA-No.

```

FEATURES

```

source
1. 548
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CO-1v-e-09-0-01"
/clone_lib="UI-R-CO"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; The UI-R-CO
library is a subtracted library derived from the UI-R-A1
and UI-R-E1 libraries. The UI-R-A1 library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, and muscle. The UI-R-E1
library consisted of a mixture of individually tagged
normalized libraries constructed from 8, 12 and 18-day
embryos. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dT track which
allows identification of the library of origin of a clone
within the mixture. The subtracted library (UI-R-CO) was
constructed as follows: PCR amplified cDNA inserts from a
pool of UI-R-A1 and UI-R-E1 clones from which 3' ESTs had
been derived was used as a driver in a hybridization with
the pooled UI-R-A1 and UI-R-E1 library in the form of
single-stranded circles. The remaining single-stranded
circles (subtracted library) was purified by
hydroxyapatite column chromatography, converted to
double-stranded circles and electroporated into DH10B
bacteria (Life Technologies) to generate the UI-R-CO
library. This procedure has been previously described
(Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
1996)."
BASE COUNT      99 a      154 c      137 g      157 t      1 others
ORIGIN

```

```

Query Match      38.3% Score 472.6; DB 46; Length 548;
Best Local Similarity 94.9%; Pred. No. 4e-78;
Matches 522; Conservative 0; Mismatches 20; Indels 8; Gaps 3;

```

```

OY 677 CGGCCGCTGAGAGCTGTCTGCCAGCCGATGTGGCGCGTGGCGGAGAACTTG 736
|||||
DB 1 CGGCCGCTGAGAGCTGTCTGCCAGCCGATGTGGCGCGTGGCGGAGAACTTG 60
|||||
OY 737 GCGCGATCCCTCTTAACCGGACTCCGAGTACTAGTCTCCCTCCGAGATC 796
|||||
DB 61 GCGCGATCCCTCTTAACCGGACTCCGAGTACTAGTCTCCCTCCGAGATC 120

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/clone="IMAGE:642191"
/clone.lib="Soares 2NbMT"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - Oligo(dT) primer [5',
TGTTACCAATCTGAGTAGGGAGCGCCGCTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT      75 a      230 c      167 g      83 t
ORIGIN

Query Match          36.8%; Score 454.8; DB 30; Length 555;
Best Local Similarity 92.8%; Pred. No. 7.8e-75;
Matches 477; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY   70 CACCGGAGCGCGCGGTACTGCTGTCTTCCTCCCCCATCAGAGCGGCCGCGAGCGTATG 129
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   42 CCCCAGAGCCCCCAGCCGCGGCTCCCGCGCTGCGCCAGCGCACCCCGGAGCGTATG 101

QY   130 GCCCACCCTTCACACTGSGCCCTCGAGTAGAGTAGTACAGCAACAGTGGACCGGA 189
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   102 GCCCACCCTTCACACTGSGCCCTCGAGTAGAGTAGTACAGCAACAGTGGACCGGA 161

QY   190 CAATGCATCTCCCGGAGCAGAGCCCCGAGCGGGGTCAAGACCTCTCTGCTGTC 249
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   162 CAATGCATCTCCCGGAGCAGAGCCCCGAGCGGGGTCAAGACCTCTCTGCTGTC 221

QY   250 TTTCGTCCTGCGACGCGCGCCGCTGCGTCCCGCGCCCGCGCGGGGTCCAGCCCGCAGC 309
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   222 TTTCGTCCTGCGACGCGCGCCGCTGCGTCCCGCGCCCGCGGGGTCCAGCCCGCAGC 281

QY   310 CCTGCGACACTGACTCTCCGACCTTCCGCTCCACTCCGATTACCGGGGACATCAGCG 369
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   282 CCTGCGACACTGACTCTCCGACCTTCCGCTCCACTCCGATTACCGGGGACATCAGCG 341

QY   370 GACGAGCGGCTCTGTGAGCGCCTGCGGCTTATTGGGGACCCCTGAGCGTGCAGGGGCG 429
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   342 GACGAGCGGCTCTGTGAGCGCCTGCGGCTTATTGGGGACCCCTGAGCGTGCAGGGGCG 401

QY   430 GCACGAGGCGGTGCGTGGCGGAGCCCGTGGGACCTCTTGTGGCGGACATGCTCAACG 489
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   402 GCACGAGGCGGTGCGTGGCGGAGCCCGTGGGACCTCTTGTGGCGGACATGCTCAACG 461

QY   490 GAATGCTTTTCGCGCTCAGCGTGAAGATGGCTTCGGGGCCCGACAGACATCGCGGTCA 549
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   462 GAATGCTTTTCGCGCTCAGCGCTGAAGATGGCTTTGGGGCCCGACAGACATCGCGGTCA 521

QY   550 CTTCAGGCGCGCGCTTCACTTGAGCGGACG 583
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   522 CTTCATGCGCGGCGCTTCACTTGAGCGGACG 555

RESULT           9
LOCUS            AA850220
DEFINITION       ESRI92987 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
VERSION          AA850220.1 GI:4131808
KEYWORDS         EST.
SOURCE           Rattus sp.
ORGANISM         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                  Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus.
```


REFERENCE 1 (bases 1 to 523)
 AUTHORS Lee, N.H., Glodex, A., Chandra, I., Mason, T.M., Quackenbush, J.,
 Kertavage, A.R. and Adams, M.D.
 TITLE Rat Genome Project: Generation of a Rat EST (BEST) Catalog & Rat
 Gene Index
 JOURNAL Unpublished (1998)
 COMMENT On Jul 19, 1995 this sequence version replaced gi:2937760.
 Other ESTs: EST192988
 Contact: Lee, NH
 ATCC
 The Institute for Genomic Research
 9712, Medical Center Drive, Rockville, MD 20850, USA
 Tel: (301)-838-3529
 Fax: (301)-838-0208
 Email: nhlee@tigr.org
 Seq primer: M13-21.
 Location/Qualifiers
 source 1..523
 /organism="Rattus sp."
 /db_xref="ATCC (Inhost):2008691"
 /db_xref="taxon:10118"
 /clone="ROYAB05"
 /clone_1id="Normalized rat ovary, Bento Soares"
 /note="Organ: ovary; Vector: pT73Pac; Site_1: EcoRI;
 Site_2: NotI"
 BASE COUNT 88 a 147 c 132 g 156 t
 ORIGIN

Query Match 36.4%; Score 449.4; DB 45; Length 523;
 Best Local Similarity 94.5%; Pred. No. 7.8e-74;
 Matches 500; Conservative 0; Mismatches 21; Indels 8; Gaps 3;

OY 685 GAGAGAGCTGTGTCGCCAGCGCATGTGCGCGCGTGGTCCGAGAACCTGCGCGCAT 744
 DB 1 CGAGCGCTGTGTCCCGACGCGCATGTGCGCGCGTGGTCCGAGAACCTGCGCGCAT 60
 OY 745 CCCTTTAACCCCGTACTCCGTACTACTAGTTCCTTCCCTCCAGANTGACCGGC 804
 DB 61 CCCTTTAACCCCGTACTCCGTACTACTAGTTCCTTCCCTCCAGANTGACCGGC 120
 OY 805 TCCCGCTGTG-CGCGAGCATTAAGTGGGGCGCTTATTATTCTTATTATTATTATTA 863
 DB 121 TGCCCGCTGTGCGCGAGCATTAAGTGGGGCGCTTATTATTCTTATTATTATTATTA 180
 OY 864 TTATTTTCTGGAACAGGTGGAGCCCTCCCGCTGGGTGGAGGGAGGTGTGGA 923
 DB 181 TTATTTTCTGGAACAGGTGGAGCCCTCCCGCTGGGTGGAGGGAGGTGTGGA 240
 OY 924 GGGTAGATGCTCCCTCCACTTCTGCTGAGAGACCTATCCACCTCTCAGGGGTGGGGTG 983
 DB 241 GGGTAGATGCTCCCTCCACTTCTGCTGAGAGACCTATCCCGCTCTC-----GGGGGGC 294
 OY 984 CTCCTCTCTGTGCTCCCTCCCGGTCCCGCTGTGTGAGACGTTGTGTGGGCCA 1043
 DB 295 CTCCTCTCTGTGCTCCCTCCCGGT-CCCGCTGTGTGAGAGGTTGTGTGGGGCCA 353
 OY 1044 GGACCTGATTCCTACTCTACCTCTCAGAGTTTACATATTCACCTACTTTCGACAAAC 1103
 DB 354 GGACCTGATTCCTACGCTACTCTCTCATGTTTACATGTTCCCACTATCTTGCACAAAC 413
 OY 1104 CAGGGCTGGGGAGGCTCTGGCTTCATTTTCTGCTGTGAGAAATATCCATTATTATA 1163
 DB 414 CAAGGCTGGGGAGGCTCTGGCTTCATTTTCTGCTGTGAGAAATATTCAGTTATA 473
 OY 1164 TTTTACAGCCAGTTAGTAAATTAATTATTATGAAGTTTTTTTT 1212
 DB 474 TTTTACATCCAGTTAGTAAATTAATTATTATGAAGTTTTTTTT 522

RESULT 10
 AA024269/c 462 bp mRNA EST 21-JAN-1997
 LOCUS

DEFINITION mh99h07.r1 Soares mouse placenta 4MBP13.5 14.5 Mus musculus cDNA
 clone IMAGE:459133 5', mRNA sequence.
 ACCESSION AA024269
 VERSION GI:1489155
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 462)
 AUTHORS Maria, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Stepien, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Maria M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:276021
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 442.
 Location/Qualifiers
 source 1..462
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:459133"
 /clone_1id="Soares mouse placenta 4MBP13.5 14.5"
 /sex="unknown"
 /tissue_type="placenta"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: placenta; Vector: pT73D-Pac (Pharmacia)
 with a modified polylinker. Site_1: Not I; Site_2: Eco RI;
 1st strand cDNA was primed with a Not I - oligo(dt) primer
 [5'
 TGTACCAATCTGAAGTGGAGCGCGCGGAGAAATTTTTTTTTTTTTTTTTTTT
 T 3']; double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M.Fatima Bonaldo."
 BASE COUNT 149 a 110 c 117 g 85 t 1 others
 ORIGIN

Query Match 35.8%; Score 441.8; DB 27; Length 462;
 Best Local Similarity 97.2%; Pred. No. 2e-72;
 Matches 449; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 759 TATCCCGGATACCTAGTTCCTTCCCTCCGATCTACCGCGCTGGCGGC 818
 DB 462 TATCCCGGATACCTAGTTCCTTCCCTCCGATCTACCGCGGTATGCGGC 403
 OY 819 AGCATTAAGTGGGGCGCCCTATTATTCTTATTATTATTATTATTATTCTGGAAC 878
 DB 402 ACTTNTAAGTGGGGCGCCCTATTATTCTTATTATTATTATTATTATTCTGGAAC 343
 OY 879 CACGTGGAGGCTCCCTCCCGCTGGGTGGAGGAGTGGTGGAGGAGTGCCTCC 938
 DB 342 CACGTGGAGGCTCCCTCCCGCTGGGTGGAGGAGTGGTGGAGGAGTGCCTCC 283
 OY 939 CACTTCTGGCTGGAGACTATCCACCTCTCAGGGGTGGGGGTCTCCCTCTGTGC 998
 DB 282 CACTTCTGGCTGGAGACTATCCACCTCTCAGGGGTGGGGGTCTCCCTCTGTGC 223

Oy	999	TCCCTCCGGGGTCCCCCGTGGTTGAGACGTTGTGCTGGGGCAGAGACTGAATTCAC	1058
Db	222	ATCTCTGGGGTCCCCCGTGGTTGAGACGTTGTGCTGGGGCAGAGACTGAATTCAC	163
Oy	1059	TCTACACTCTGCATGTTACATATTCCAGTACTTTGGCACAACAGGGGTGGGGGAGG	1118
Db	162	TCTACACTCTGCATGTTACATATTCCAGTACTTTGGCACAACAGGGGTGGGGGAGG	103
Oy	1119	GTCCTCTGGCTCATTTTTCGCTGTGCGAATAATCTATTATATTTTACAGCCAGTT	1178
Db	102	GTCCTCTGGCTCATTTTTCGCTGTGCGAATAATCTATTATATTTTACAGCCAGTT	43
Oy	1179	TAGGTAATTAACCTTATTATGAAAGTTTTTTTAAAGAAA	1220
Db	42	TAGGTAATTAACCTTATTATGAAAGTTTTTTTAAAGAAA	1

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RESULT 11
AI400249/c
LOCUS      AI400249      591 bp      mRNA      EST      30-MAR-1999
DEFINITION t668d01.x1 Soares.Nhnpu.S1 Homo sapiens cDNA clone IMAGE:2113921
            ; similar to TR:015097 015097 JAB. PRR1AL CDS ; contains MER22.b
            MS1 repetitive element ;; mRNA sequence.
AI400249
ACCESSION

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ACCESSION	AI400249	
VERSION	AI400249.1	GI:4243336
KEYWORDS	EST.	
SOURCE	human.	

SOURCE	human
ORGANIZATION	...

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 591)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
On Mar 20, 1998 this sequence version replaced gi:2980432.

Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert length: 816 Std Error: 0.00
 Seq primer: -400P from GIBCO
 High quality sequence stop: 465.
 Location/Qualifiers

FEATURES	Location/Qualifiers
source	1. .591

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2113921"
/clone_1fb="Soares NbHMPu.51"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/notes="Organ: mixed (see below); Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHx, pregnant uterus
NbHPU, and fetal heart NbHH19w) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."

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BASE COUNT	87 a	185 c	241 g	74 t	4 others
ORIGIN					

Query Match	34.1%	Score 421.4	DB 46	Length 591
Best Local Similarity	87.0%	Pred. NO. 1.2e-68		
Matches 507; Conservative	0	Mismatches 70	Indels 6	Gaps 4

OY	101	CCCCATCAGGCGACGCCCGGAGCGCTATGATGCCACCCCTCCAGCTGGGCCCCCTCCAGATAGG	160
Db	577	CCCCCGGCACGCGACCCGGGGAGCG-TATGGGCCACCCCTCCGGGCTGGCCCCCTTCTGTAGN	519
OY	161	ATGGTAGACGCGCAACAGAGTGGAGCGCCGCAATATGCAATCTCCCGGCGACAGAGCCCCGA	220
Db	518	ATGGTAGAGC-CAACAGAGTGGCCAGCGCGAATAATGCAGTCT-CCGACAGACAGAGCCCCGA	461
OY	221	CGCGGGTTCAGAGCCCTCTCTGTCTCTGTCTGTCTGTCTGTCCACAGCGGCCCCCGTGGCTCC	280
Db	460	CGNCGGCGCAGAAC---CTCCCTNCTTCTTNCCTTCTTCCGCCCGCGGCCCGCGCGGCCG	404
OY	281	CGGCGCTCGCGCGGGGGTGGCCAGCGCCGACGCCCTGGGGGNACTACATTCGCGACCTCCG	340
Db	403	CGGCGGTGCCCCCGGGGTCCCGGCCCCGGCCCCCGGGGAGACGCAATTCGCGACATTCGT	344
OY	341	TCCCACTCCGATTACCGGGCGCATCACGCGGAGACAGCGCGCTCTGGAGCGCTCGGGCTTC	400
Db	343	TGCGACGCGCATTTACCGGGCGCATCACGCGCGCCGCGACGCGCTCTGTGAGAGCCTTCGGGATT	284
OY	401	TATTGGGAGACCCCTGAGCGGTGCACGGGGGCGCACAGAGCGGCTGCTGCCAGACCCGTGGGC	460
Db	283	TACTGGGGGGCCCCCTGAGCGTGCACAGGGGGGCGACAGAGCGGCTTCGCGCGACCCGTGGGC	224
OY	461	ACCTTCCTGGGGGCGCAGATGCTCAACGGAATGCTTTGGGCGCTGAGGTAAGTG	520
Db	223	ACCTTCCTGGGGGCGCAGACCGCGCAGCGGAATGCTTTTGGCTTATGAGTAAGTG	164
OY	521	GCTTCGGGGCCCAAGAGCATCCGCTGTGACATTCACAGGCGCGCGCTTCCATTTGAGAGGC	580
Db	163	GCCTCGGGAGCCAGAGACATCCGCGGTGACATTCACAGCGCGCGCTTCCACTGTGATGCG	104
OY	581	AGCGCGAGACCTTGCACTGCTTTTCAGACTGCTGGAGACACTACGTGGCGGCGCGCGC	640
Db	103	AGCGCGAGAGCTTGCACTGCTTCTTTCAGAGTGTGAGACACTACGTGGCGGCGCGCGC	44
OY	641	CGCATGTTGGGGGCCCCGCTGCGCCAGCGCCCGCGTGGCGCGC	683
Db	43	CGCATGTTGGGGGCCCCGCTGCGCCAGCGCCCGCGTGGCGCGC	1

RESULT	12
AA119130/c	
LOCUS	
DEFINITION	
AA119130	449 bp mRNA
mp66e04.r1 Soares	EST
2NDMT Mus musculus	CDNA clone IMAGE:574206
5'	
sequence.	

ACCESSION	AA119130
VERSION	AA119130.1
REMARKS	GI:1676621
DATE	

KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus

REFERENCE
1 (bases 1 to 449)
Matra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Euthayola, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

TITLE The WASHU-HHMT Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT On Sep 12, 1996 this sequence version replaced g1:1407492

Contact: Maira M/Mouse EST Project
WashU-NHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel.: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:348834
Seq primer: -28M13 rev2 from Amersham

34.08; Score 419.8; DB 27; Length 493;

Location/Qualifiers
1. .436

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/organism="Mus musculus"  
/strain="C57BL/6J"  
/db_xref="taxon:10090"  
/clone_image:577342"  
/clone_lib="Soares 2NDMT"  
/sex="male"  
/tissue_type="thymus"  
/dev_stage="4 weeks"  
/lab_host="DH10B"  
/note="Vector: pT773D-Pac (Pharmacia) with a modified  
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer [5'  
TGTTCACATCTGAGTGGAGCGCGCGTGTGTGTGTGTGTGTGTGTGT  
3']; double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT773 vector. RNA  
provided by Dr. Bertrand Jordan. Library went through two  
rounds of normalization, and was constructed by Bento  
Soares and M.Fatima Bonaldo."
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BASE COUNT 53 a 184 c 127 g 72 t

ORIGIN

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Query Match 33.3%; Score 410.8; DB 28; Length 436;  
Best Local Similarity 99.1%; Pred. No. 1.1e-66;  
Matches 434; Conservative 0; Mismatches 2; Indels 2; Gaps 2;  
  
QY 8 CAAAGCTCCGCGGGGATTCGCGTCTGCGCTCTTGGGGTCTGTGGCGGCTGT 67  
DB 1 CAAAGCTCCGCGGGGATTCGCGTCTGCGCTCTTGGGGTCTGTGGCGGCTGT 60  
  
QY 68 GCACACCGGAGCGCGGCTCAGTGCCTGTCTGCCCATCAGCGCAGCGCGACGCTA 127  
DB 61 GCACACCGGAGCGCGGCTCAGTGCCTGTCTGCCCATCAGCGCAGCGCGACGCTA 120  
  
QY 128 TGCCCAACCCCTTCAGACTGCCCCCTGAGTAGAGTAGAGCAACAGAGGTGGCAGCC 187  
DB 121 TGCCCAACCCCTTCAGACTGCCCCCTGAGTAGAGTAGAGCAACAGAGGTGGCAGCC 180  
  
QY 188 GACATAGCATCTCCCGGAGCAGAGCCCGAGCGGCTCAGAGCCCTCTGCTCTCG 247  
DB 181 GACATAGCATCTCCCGGAGCAGAGCCCGAGCGGCTCAGAGCCCTCTGCTCTCG 240  
  
QY 248 TCTTGCTCTGCGAGCGGCGCGCTGCGCTCCCGGCGCTGCGCGGCTCCAGGCCCA 307  
DB 241 TCTTGCTCTGCGAGCGGCGCGCTGCGCTCCCGGCGCTGCGCGGCTCCAGGCCCA 298  
  
QY 308 GCCCCTGGGACACTCTTCGACACTTCGCTCCACTCCGATTACCGGCGCATCAG 367  
DB 299 GCCCCTGGGACACTCTTCGACACTTCGCTCCACTCCGATTACCGGCGCATCAG 358  
  
QY 368 CGGACACGCGGCTCTGAGCGCTGCGGCTCTATTGGGACCCCTGAGCGTGCACGGG 427  
DB 359 CGGACACGCGGCTCTGAGCGCTGCGGCTCTATTGGGACCCCTGAGCGTGCACGGG 418  
  
QY 428 GCGCAGAGCGGCTGGGT 445  
DB 419 GCGCAGAGCGGCTGGGT 436
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